



PLANT AND ANIMAL SCIENCES: AGRIGENOMICS

Accurate and actionable data to drive agriculture

Unravel the complexity of plant and animal genomes with HiFi sequencing to harness agrigenomics insights for breeding, protection, and genome engineering workflows to feed a growing population.

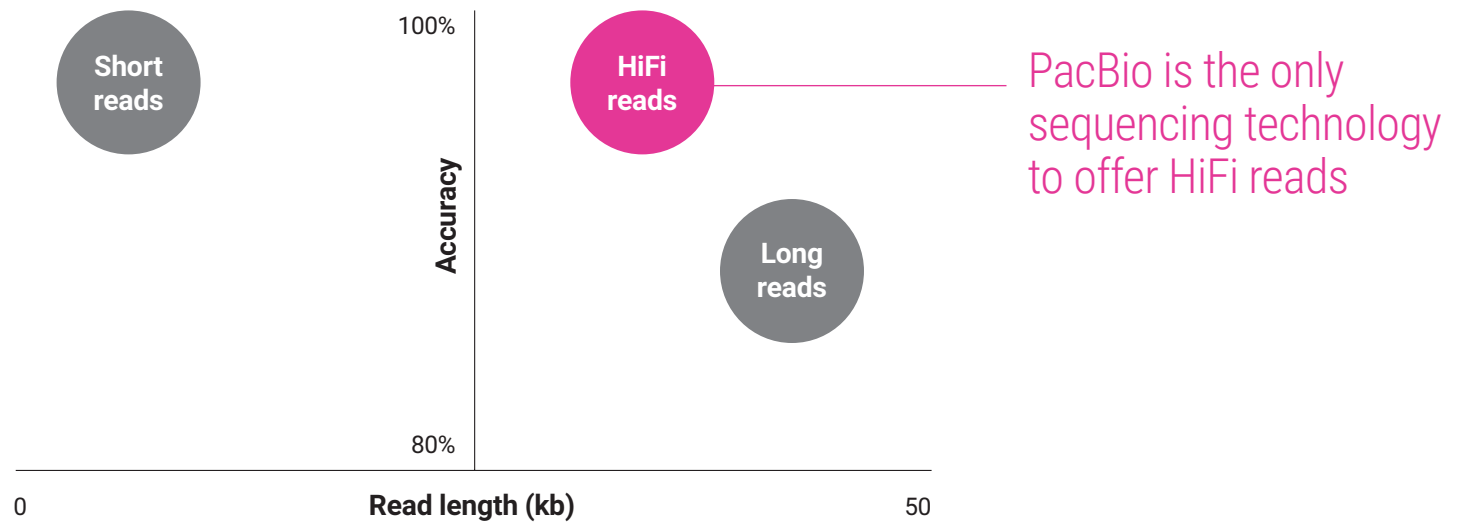
Utilizing agrigenomics to tackle global challenges

As the world population grows and climate patterns change, scientists are turning to modern genomics technology to sustainably meet a growing demand to feed the world. PacBio provides cutting-edge sequencing solutions that enable agricultural scientists to discover and harness biological information. Scientists can use these biological insights to enhance marker development, facilitate the production of more nutritious food, protect crop and livestock health, and increase agricultural yield.

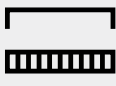



HiFi sequencing for the best of long *and* short reads

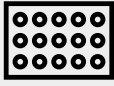
With PacBio HiFi sequencing you no longer have to compromise between long read lengths and high accuracy.





The benefits of HiFi reads


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Long read lengths up to 25 kb
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High read accuracy (99.9%)
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Easy library preparation
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Low coverage requirements
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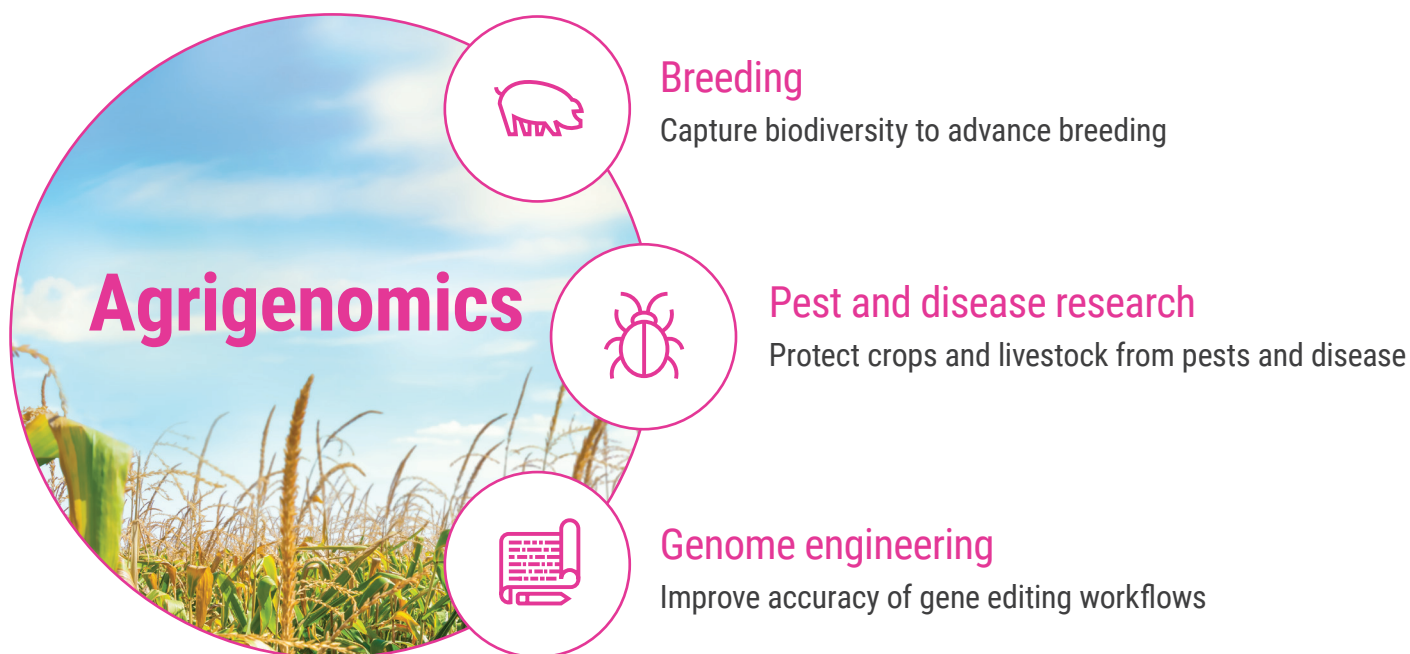
Small file sizes to minimize compute time
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A single technology solution for a range of applications

A typical 20,000 bp HiFi read has ~8 incorrect bases



Agrigenomics data in action



Applications to fuel agrigenomics



Whole genome sequencing

Produce reference-quality genomes with phased haplotypes from even small-bodied organisms



Structural variant calling

Use high-sensitivity variant calls with low false discovery rate to gain actionable insights across populations



Targeted sequencing

Choose from flexible options to target regions to access to all variants even in the most complex regions



RNA sequencing

Access full-length transcript sequences to identify novel genes and transcripts and improve genome annotation



Complex populations

Comprehensively characterize metagenomes with long, highly accurate, single-molecule reads – no assembly required



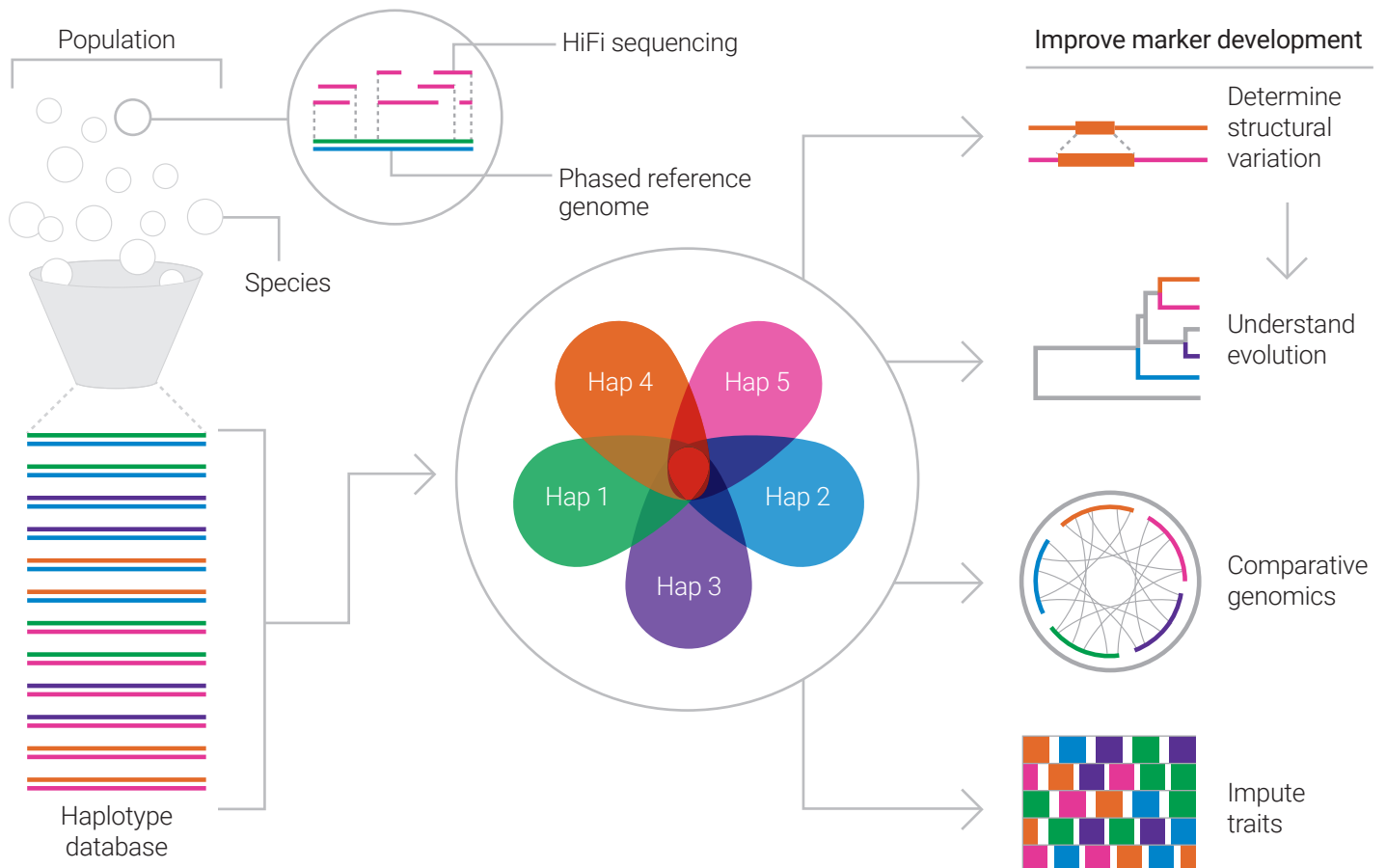
Agrigenomics for breeding programs

Build haplotype-resolved pangenomes to drive marker development, trait discovery, and germplasm characterization

- Build reference-quality, haplotype-resolved pangenomes for breeding
- Impute desirable traits to SNPs, structural variants, and complex genotypes
- Capture genomic variants on a genome-wide scale for outbreds, inbreds, and populations

Whole genome sequencing has provided breeders with data-driven strategies for marker-assisted selection by identifying desirable traits. However, within the complex biology of plants and animals, these traits are often too complex to use single SNPs for imputation and require an understanding at a complete haplotype scale.

Because HiFi sequencing is single-molecule in nature, highly accurate, and read lengths span many kilobases, you can now quickly assemble phased, reference-quality genomes for even the most complex plant and animal genomes. With third-generation sequencing tools, researchers have been able to better impute complex traits involved in climate adaptation, pest and pathogen disease resistance, and health.





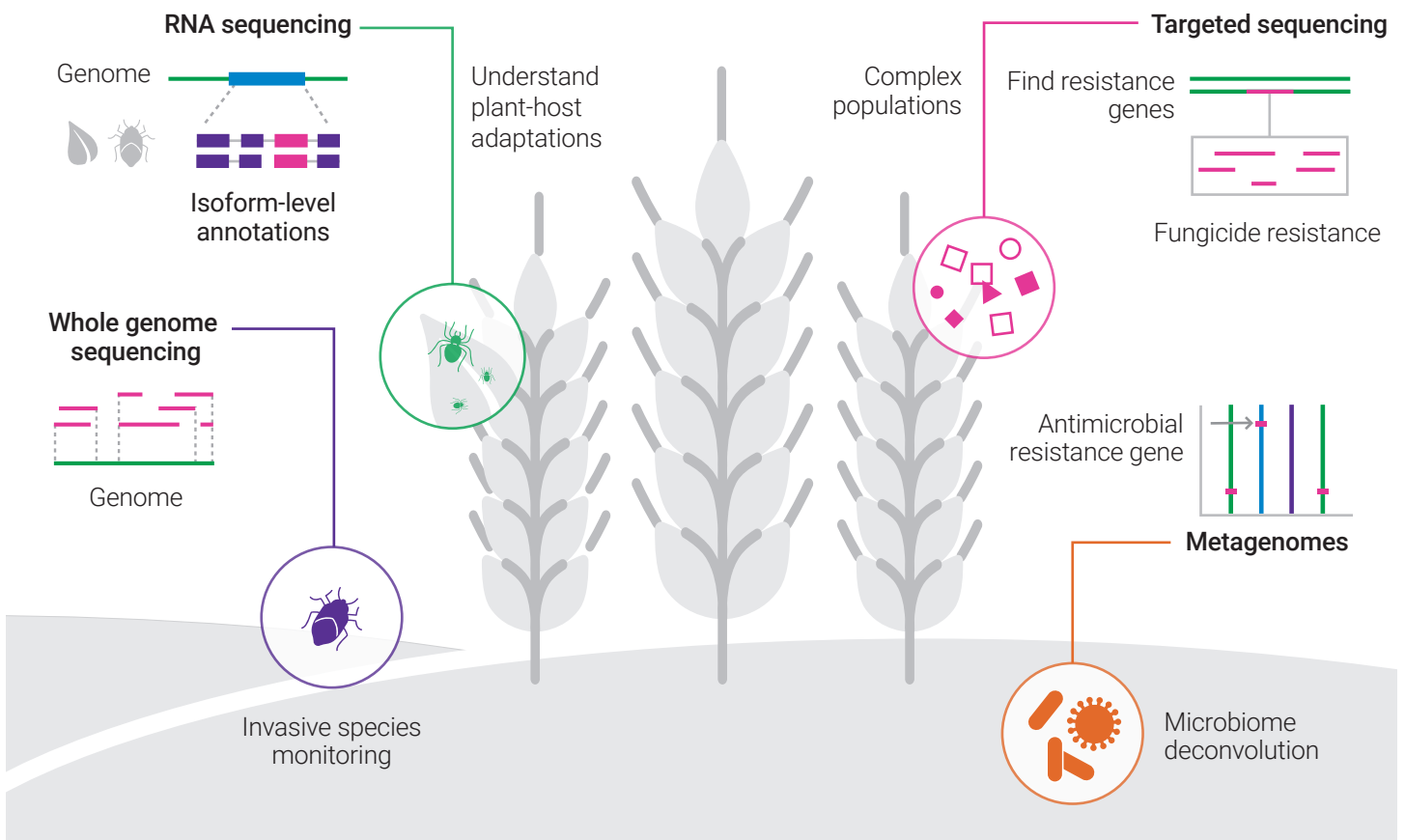
Agrigenomics for pest and disease research

Identify genomic strategies to protect crop and livestock health

- Capture pest diversity on the molecular level
- Generate complete genome assemblies from just 5 ng of DNA input
- Build annotations to better understand gene function

Find genomic clues hidden in the highly variable genetics of organisms such as insects, weeds, and fungi harming agricultural yield to tackle pests on the molecular level.

Insects, fungi, invasive species, and agricultural pests can have shorter life cycles and rapidly reproduce, resulting in highly variable genetics within single populations. HiFi sequencing equips researchers with the technology to dig into genomes and transcriptomes to find novel genes responsible for immunity, metabolic detoxification, and resistance to pesticides.





Agrigenomics for genome engineering programs

Sequencing tools for a new paradigm in agriculture

- Speed up design workflows with accurate reference genomes
- Find splice variants within the transcriptome
- Validate edited sites
- Determine structural rearrangements across chromosomes

Discover, design, and validate genome engineering workflows with confidence, ease, and sensitivity.

Agriscientists know that to feed the estimated 10 billion people who will be living on the planet in 2050,⁹ a variety of different programmable molecular techniques are needed to increase our food supply. Whether you need a better reference genome to design your editing experiment, or sequence data to validate constructs, confirm edits, and evaluate off-target effects, HiFi sequencing provides a fast, reliable solution.



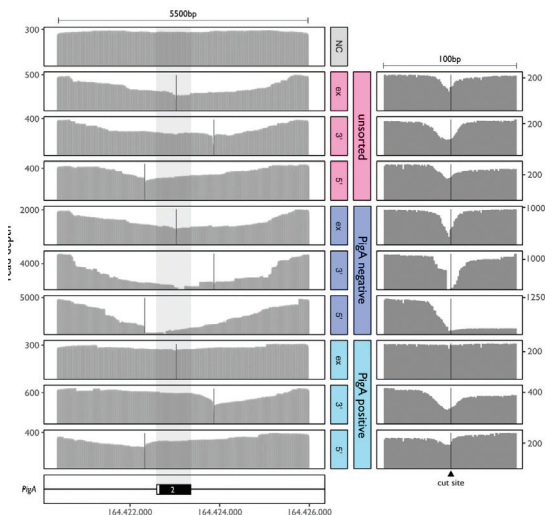
Better reference genomes for better editing

Scientists used PacBio whole genome sequencing to assess on-target and off-target integration of the donor template effects in **CRISPR edited calf**.¹⁰

Sequence beyond your target

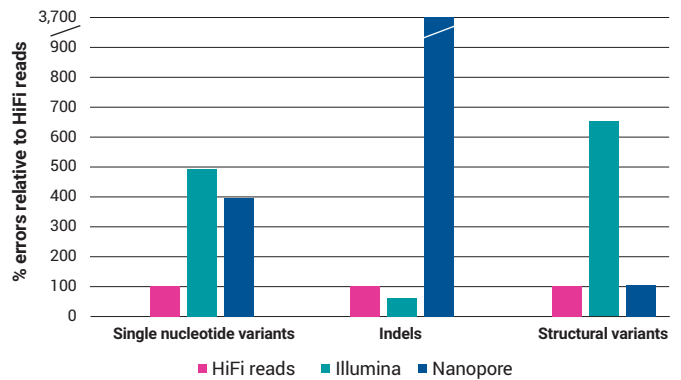
Understanding the extent of CRISPR-Cas9 editing requires long read lengths and high accuracy to capture both on- and off-target effects to fully evaluate editing outcomes on a targeted and genome-wide scale.

Targeted validation



Analysis of the PigA locus edited with the CRISPR-Cas9 method using selected gRNAs. SMRT® sequencing of a 5.5 kb amplicon around gRNA cut sites (vertical lines) enabled detection of large-scale deletions and structural changes missed by other methods¹¹

Comprehensive variant detection



Variant calling performance against *Genome in a Bottle* benchmarks for PacBio HiFi reads (35-fold, Sequel II system, 2.0 chemistry); Illumina (35-fold, NovaSeq); Oxford Nanopore (60-fold, PromethION R9.4.1.)



Workflow

With easy-to-use, high-throughput sequencing, you can get the accuracy you need at an affordable cost



Sample prep

Flexible DNA input requirements down to 5 ng



Library prep

Adjustable multiplexing options to maximize throughput



SMRT[®] sequencing

Run up to four SMRT[®] Cells 25M at a time with the option to load the next run while the current one is sequencing



Data analysis

Use SMRT[®] Link, or open-source tools to analyze your HiFi data

This scalable workflow allows for sequencing 1,000s to 10,000s of genomes per year





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READY TO GET STARTED WITH HIFI SEQUENCING?



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